

## SEQUENCE LISTING

<110> Bennett, Michele  
Brodbeck, Robbin  
Krause, James

<120> Chimeric Neuropeptide Y Receptors

<130> N2000.001

<140> Not Yet Assigned

<141> 2000-01-28

<160> 31

<170> PatentIn Ver. 2.1

<210> 1

<211> 1605

<212> DNA

<213> Homo sapiens

<400> 1

```

ccttcttttaa tgaagcagga gcgaaaaaga caaattccaa agaggattgt tcagttcaag 60
ggaatgaaga attcagaata attttggttaa atggattcca atatggggaa taagaataag 120
ctgaacagtt gacctgcttt gaagaaacat actgtccatt tgtctaaaat aatctataac 180
aaccaaaacca atcaaaatga attcaacatt attttcccag gttgaaaatc attcagtcca 240
ctctaatttc tcagagaaga atgcccagct tctggctttt gaaaatgatg attgtcatct 300
gcccttggcc atgatattta ccttagctct tgcttatgga gctgtgatca ttcttgggtg 360
ctctggaaac ctggccttga tcataatcat ctgaaacaa aaggagatga gaaatgttac 420
caacatcctg attgtgaacc ttctcttctc agacttgctt gttgccatca tgtgtctccc 480
ctttacattt gtctacacat taatggacca ctgggtcttt ggtgaggcga tgtgtaagtt 540
gaatcctttt gtgcaatgtg tttcaatcac tgtgtccatt ttctctctgg ttctcattgc 600
tgtggaacga catcagctga taatcaaccc tcgagggtgg agaccaaata atagacatgc 660
ttatgtagggt attgctgtga tttgggtcct tgctgtggct tcttctttgc ctttctgat 720
ctaccaagta atgactgatg agccgttcca aaatgtaaca cttgatgcgt acaaagacaa 780
atacgtgtgc tttgatcaat ttccatcgga ctctcatagg ttgtcttata ccaactctct 840
cttgggtgctg cagtattttg gtccactttg ttttatattt atttgctact tcaagatata 900
tatacgcccta aaaaggagaa acaacatgat ggacaagatg agagacaata agtacagggtc 960
cagtgaaaacc aaaagaatca atatcatgct gctctccatt gtggtagcat ttgcagtcgt 1020
ctggctccct cttaccatct ttaacactgt gtgtgattgg aatcatcaga tcattgctac 1080
ctgcaaccac aatctgttat tctgtctctg ccacctcaca gcaatgatat ccacttgtgt 1140
caaccccata ttttatgggt tctgaacaa aaacttccag agagacttgc agttcttctt 1200
caacttttgt gatttccggt ctcggtatga tgattatgaa acaatagcca tgtccacgat 1260
gcacacagat gtttccaaaa cttctttgaa gcaagcaagc ccagtcgcat ttaaaaaaat 1320
caacaacaat gatgataatg aaaaaatctg aaactactta tagcctatgg tcccggatga 1380
catctgttta aaaacaagca caacctgcaa catactttga ttacctgttc tccaaggaa 1440
tggggttgaa atcatttgaa aatgactaag attttcttgt cttgcttttt actgcttttg 1500
ttgtagttgt cataattaca tttggaacaa aaggtgtggg ctttgggggtc ttctggaaat 1560
agttttgacc agacatcttt gaagtgcctt ttgtgaattt accag 1605

```

<210> 2

<211> 384

<212> PRT

<213> Homo sapiens

<400> 2

Met Asn Ser Thr Leu Phe Ser Gln Val Glu Asn His Ser Val His Ser  
1 5 10 15

Asn Phe Ser Glu Lys Asn Ala Gln Leu Leu Ala Phe Glu Asn Asp Asp  
20 25 30

Cys His Leu Pro Leu Ala Met Ile Phe Thr Leu Ala Leu Ala Tyr Gly  
35 40 45

Ala Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile  
50 55 60

Ile Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu Ile Val  
65 70 75 80

Asn Leu Ser Phe Ser Asp Leu Leu Val Ala Ile Met Cys Leu Pro Phe  
85 90 95

Thr Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu Ala Met  
100 105 110

Cys Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile  
115 120 125

Phe Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn  
130 135 140

Pro Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Val Gly Ile Ala  
145 150 155 160

Val Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Leu Ile Tyr  
165 170 175

Gln Val Met Thr Asp Glu Pro Phe Gln Asn Val Thr Leu Asp Ala Tyr  
180 185 190

Lys Asp Lys Tyr Val Cys Phe Asp Gln Phe Pro Ser Asp Ser His Arg  
195 200 205

Leu Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu  
210 215 220

Cys Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg  
225 230 235 240

Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser  
245 250 255

Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val Ala Phe  
260 265 270

Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe Asp Trp  
275 280 285

Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe Leu Leu  
290 295 300

Protein Data Bank

Cys His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile Phe Tyr  
 305 310 315 320  
 Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Phe Asn  
 325 330 335  
 Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met  
 340 345 350  
 Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser  
 355 360 365  
 Pro Val Ala Phe Lys Lys Ile Asn Asn Asn Asp Asp Asn Glu Lys Ile  
 370 375 380

<210> 3  
 <211> 382  
 <212> PRT  
 <213> Rattus norvegicus

<400> 3  
 Met Asn Ser Thr Leu Phe Ser Arg Val Glu Asn Tyr Ser Val His Tyr  
 1 5 10 15  
 Asn Val Ser Glu Asn Ser Pro Phe Leu Ala Phe Glu Asn Asp Asp Cys  
 20 25 30  
 His Leu Pro Leu Ala Val Ile Phe Thr Leu Ala Leu Ala Tyr Gly Ala  
 35 40 45  
 Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile Ile  
 50 55 60  
 Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu Ile Val Asn  
 65 70 75 80  
 Leu Ser Phe Ser Asp Leu Leu Val Ala Val Met Cys Leu Pro Phe Thr  
 85 90 95  
 Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu Thr Met Cys  
 100 105 110  
 Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile Phe  
 115 120 125  
 Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn Pro  
 130 135 140  
 Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Ile Gly Ile Thr Val  
 145 150 155 160  
 Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Val Ile Tyr Gln

165										170					175				
Ile	Leu	Thr	Asp	Glu	Pro	Phe	Gln	Asn	Val	Ser	Leu	Ala	Ala	Phe	Lys				
			180					185					190						
Asp	Lys	Tyr	Val	Cys	Phe	Asp	Lys	Phe	Pro	Ser	Asp	Ser	His	Arg	Leu				
	195						200					205							
Ser	Tyr	Thr	Thr	Leu	Leu	Leu	Val	Leu	Gln	Tyr	Phe	Gly	Pro	Leu	Cys				
	210					215					220								
Phe	Ile	Phe	Ile	Cys	Tyr	Phe	Lys	Ile	Tyr	Ile	Arg	Leu	Lys	Arg	Arg				
225				230				235						240					
Asn	Asn	Met	Met	Asp	Lys	Ile	Arg	Asp	Ser	Lys	Tyr	Arg	Ser	Ser	Glu				
				245				250						255					
Thr	Lys	Arg	Ile	Asn	Val	Met	Leu	Leu	Ser	Ile	Val	Val	Ala	Phe	Ala				
			260				265						270						
Val	Cys	Trp	Leu	Pro	Leu	Thr	Ile	Phe	Asn	Thr	Val	Phe	Asp	Trp	Asn				
	275						280					285							
His	Gln	Ile	Ile	Ala	Thr	Cys	Asn	His	Asn	Leu	Leu	Phe	Leu	Leu	Cys				
	290					295					300								
His	Leu	Thr	Ala	Met	Ile	Ser	Thr	Cys	Val	Asn	Pro	Ile	Phe	Tyr	Gly				
305				310				315						320					
Phe	Leu	Asn	Lys	Asn	Phe	Gln	Arg	Asp	Leu	Gln	Phe	Phe	Phe	Asn	Phe				
				325				330						335					
Cys	Asp	Phe	Arg	Ser	Arg	Asp	Asp	Asp	Tyr	Glu	Thr	Ile	Ala	Met	Ser				
			340				345						350						
Thr	Met	His	Thr	Asp	Val	Ser	Lys	Thr	Ser	Leu	Lys	Gln	Ala	Ser	Pro				
	355						360					365							
Val	Ala	Phe	Lys	Lys	Ile	Ser	Met	Asn	Asp	Asn	Glu	Lys	Ile						
	370					375					380								

<210> 4  
 <211> 1406  
 <212> DNA  
 <213> Homo sapiens

<400> 4  
 ttttggttgc tgacaaatgt ctttttattc caagcaggac tataatatgg atttagagct 60  
 cgacgagtat tataacaaga cacttgccac agagaataat actgctgcca ctcggaattc 120  
 tgatttccca gtctgggatg actataaaaag cagtgtagat gacttacagt attttctgat 180  
 tgggctctat acatttgtaa gtcttcttgg ctttatgggg aatctactta ttttaatggc 240  
 tctcatgaaa aagcgtaatc agaagactac ggtaaacttc ctcataggca atctggcctt 300  
 ttctgatata ttggttgtgc tgttttgctc acctttcaca ctgacgtctg tcttgctgga 360  
 tcagtggatg tttggcaaag tcatgtgcca tattatgcct tttcttcaat gtgtgtcagt 420  
 tttggtttca actttaattt taatatcaat tgccattgtc aggtatcata tgataaaaca 480  
 tcccatatct aataatttaa cagcaaacca tggctacttt ctgatatgcta ctgtctggac 540

```

actaggtttt gccatctgtt ctccccttcc agtggtttcac agtcttgtgg aacttcaaga 600
aacatttggt tcagcattgc tgagcagcag gtatttatgt gttgagtcac ggccatctga 660
ttcatacaga attgacctta ctatctcttt attgctagtt cagtatatcc tgcccttagt 720
ttgtcttact gtaagtcata caagtgtctg cagaagtata agctgtggat tgtccaacaa 780
agaaaaacaga cttgaagaaa atgagatgat caacttaact cttcatccat ccaaaaaagag 840
tgggcctcag gtgaaactct ctggcagcca taaatggagt tattcattca tcaaaaaaca 900
cagaagaaga tatagcaaga agacagcatg tgtgttacct gctccagaaa gaccttctca 960
agagaaccac tccagaatac ttccagaaaa ctttggtctt gtaagaagtc agctctcttc 1020
atccagtaag ttcataccag gggccccccac ttgctttgag ataaaaacctg aagaaaaattc 1080
agatgttcat gaattgagag taaaacgttc tgttacaaga ataaaaaaga gatctcgaag 1140
tgttttctac agactgacca tactgatatt agtatttgct gttagttgga tgccactaca 1200
ccttttccat gtggtaaact attttaatga caatcttatt tcaaataggc atttcaagtt 1260
ggtgtattgc atttgtcatt tgttgggcat gatgtcctgt tgtcttaatc caattctata 1320
tggtgtttctt aataatggga ttaaagctga tttagtgtcc cttatacact gtcttcatat 1380
gtaataattc tcactgttta ccaagg                                1406

```

<210> 5  
 <211> 1069  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Y5/Y1 CHIMERA

```

<400> 5
ttttgggttg tgacaaatgt ctttttattc caagcaggac tataatatgg atttagagct 60
cgacgagtat tataacaaga cacttgccac agagaataat actgctgcc ctcggaattc 120
tgatttccca gtctgggatg actataaaag cagtgtagat gacttacagt attttctgat 180
tggtctctat acatttgtaa gtcttcttgg ctttatgggg aatctactta ttttaattgc 240
tctcatgaaa aagcgtaatc agaagactac ggtaaaactt ctcataggca atctggcctt 300
ttctgataac ttggttgtgc tgttttgcct acctttcaca ctgacgtctg tcttgctgga 360
tcagtggatg tttggcaaag tcatgtgcc tattatgcct tttcttcaat gtgtgtcagt 420
tttggtttca actttaattt taatatcaat tgccattgtc aggtatcata tgataaaaca 480
tcccatatct aataatttaa cagcaaacca tggctacttt ctgatagcta ctgtctggac 540
actaggtttt gccatctgtt ctccccttcc agtggtttcac agtcttgtgg aacttcaaga 600
aacatttggt tcagcattgc tgagcagcag gtatttatgt gttgagtcac ggccatctga 660
ttcatacaga attgacctta ctatctcttt attgctagtt cagtatatcc tgcccttagt 720
ttgtcttact gtaagtcata caagtgtctg catagccta aaaaggagaa acaacatgat 780
ggacaagatg agagacaata agtacaggtc cagtagatct cgaagtgttt tctacagact 840
gaccatactg atattagtat ttgctgttag ttggatgcc ctacaccttt tccatgtggg 900
aactgatttt aatgacaatc ttatttcaaa taggcatttc aagttgggtg attgcatttg 960
tcatttggtg ggcagatgt cctgttgtct taatccaatt ctatatgggt ttcttaataa 1020
tgggattaaa gctgatttag tgtcccttat acactgtctt catatgtaa 1069

```

<210> 6  
 <211> 350  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Y5/Y1 CHIMERA

```

<400> 6
Met Ser Phe Tyr Ser Lys Gln Asp Tyr Asn Met Asp Leu Glu Leu Asp
  1             5             10             15

```

Glu Tyr Tyr Asn Lys Thr Leu Ala Thr Glu Asn Asn Thr Ala Ala Thr  
 20 25 30  
 Arg Asn Ser Asp Phe Pro Val Trp Asp Asp Tyr Lys Ser Ser Val Asp  
 35 40 45  
 Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu Leu  
 50 55 60  
 Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Leu Met Lys Lys Arg  
 65 70 75 80  
 Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser  
 85 90 95  
 Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val  
 100 105 110  
 Leu Leu Asp Gln Trp Met Phe Gly Lys Val Met Cys His Ile Met Pro  
 115 120 125  
 Phe Leu Gln Cys Val Ser Val Leu Val Ser Thr Leu Ile Leu Ile Ser  
 130 135 140  
 Ile Ala Ile Val Arg Tyr His Met Ile Lys His Pro Ile Ser Asn Asn  
 145 150 155 160  
 Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr Leu  
 165 170 175  
 Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val Glu  
 180 185 190  
 Leu Gln Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Arg Tyr Leu Cys  
 195 200 205  
 Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile Ser  
 210 215 220  
 Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu Val Cys Leu Thr Val Ser  
 225 230 235 240  
 His Thr Ser Val Cys Ile Arg Leu Lys Arg Arg Asn Asn Met Met Asp  
 245 250 255  
 Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser Arg Ser Arg Ser Val Phe  
 260 265 270  
 Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp Met Pro  
 275 280 285  
 Leu His Leu Phe His Val Val Thr Asp Phe Asn Asp Asn Leu Ile Ser  
 290 295 300  
 Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu Leu Gly Met  
 305 310 315 320

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500

Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu Asn Asn Gly  
 325 330 335

Ile Lys Ala Asp Leu Val Ser Leu Ile His Cys Leu His Met  
 340 345 350

<210> 7  
 <211> 1500  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Y5/Y1 CHIMERA

<400> 7  
 atgtcttttt attccaagca ggactataat atggatttag agctcgacga gtattataac 60  
 aagacacttg ccacagagaa taatactgct gccactcgga attctgattt cccagtctgg 120  
 gatgactata aaagcagtgat agatgactta cagtattttc tgattgggct ctatacattt 180  
 gtaagtcttc ttggctttat ggggaatcta cttattttta tggctctcat gaaaaagcgt 240  
 aatcagaaga ctacggtaaa cttcctcata ggcaatctgg cttttctga tatcttggtt 300  
 gtgctgtttt gctcaccttt cacactgacg tctgtcttgc tggatcagtg gatgtttggc 360  
 aaagtcagtg gccatattat gccttttctt caatgtgtgt cagttttggg ttcaacttta 420  
 attttaatat caattgccat tgtcaggtat catatgataa aacatcccat atctaataat 480  
 ttaacagcaa accatggcta ctttctgata gctactgtct ggacactagg ttttgccatc 540  
 tgttctcccc ttccagtgtt tcacagtctt gtggaacttc aagaaacatt tggttcagca 600  
 ttgctgagca gcaggtattt atgtgttgag tcatggccat ctgattcata cagaattgcc 660  
 ttactatctt ctttattgct agttcagtat attctgccct tagtttgtct tactgtaagt 720  
 catacaagtg tctgcagaag tataagctgt ggattgtcca acaaagaaaa cagacttgaa 780  
 gaaaatgaga tgatcaactt aactcttcat ccattccaaa agagtgggct tcaggtgaaa 840  
 ctctctggca gccataaatg gagttattca ttcattcaaaa aacacagaag aagatatagc 900  
 aagaagacag catgtgtgtt acctgtcca gaaagacctt ctcaagagaa ccaactccaga 960  
 atacttccag aaaacttttg ctctgtaaga agtcagctct cttcatccag taagttcata 1020  
 ccaggggtcc ccacttgctt tgagataaaa cctgaagaaa attcagatgt tcatgaattg 1080  
 agagtaaaac gttctgttac aagaataaaa aagagatctc gaagtgtttt ctacagactg 1140  
 accatactga tattagtatt tgctgttagt tggatgccac tacacctttt ccatgtggta 1200  
 actgatttta atgacaatct tatttcaaat aggcatttca agttgggtga ttgcatattg 1260  
 catttggttg gcatgatgtc ctgttctctt aatccaattc tatatgggtt tcttaataat 1320  
 ggaattcaga gagacttgca gttcttcttc aacttttgtg atttcgggtc tcgggatgat 1380  
 gattatgaaa caatagccat gtccacgatg cacacagatg tttccaaaac ttctttgaag 1440  
 caagcaagcc cagtcgcatt taaaaaaatc aacaacaatg atgataatga aaaaatctga 1500

<210> 8  
 <211> 1201  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Y5/Y1 CHIMERA

<400> 8  
 ttttggttgc tgacaaatgt ctttttattc caagcaggac tataatatgg atttagagct 60  
 cgacgagtat tataacaaga cacttgccac agagaataat actgctgcc ctcggaattc 120  
 tgatttccca gtctgggatg actataaaa cagtgtagat gacttacagt attttctgat 180  
 tgggctctat acatttgtaa gtcttcttgg ctttatgggg aatctactta ttttaattgg 240

```

tctcatgaaa aagcgtaatc agaagactac ggtaaacttc ctcataggca atctggcctt 300
ttctgatata ttggttgtgc tgttttgctc acctttcaca ctgacgtctg tcttgctgga 360
tcagtggatg tttggcaaag tcatgtgcc aattatgcct tttcttcaat gtgtgtcagt 420
tttggtttca actttaattt taatatcaat tgccattgtc aggtatcata tgataaaaca 480
tcccatatct aataatttaa cagcaaacca tggctacttt ctgatagcta ctgtctggac 540
actaggtttt gccatctgtt ctccccttcc agtgtttcac agtcttgagg aacttcaaga 600
aacatttggt tcagcattgc tgagcagcag gtatttatgt gttgagtcac ggccatctga 660
ttcatacaga attgccttta ctatctcttt attgctagtt cagtatatct tgcccttagt 720
ttgtcttact gtaagtcata caagtgtctg catacgcta aaaaggagaa acaacatgat 780
ggacaagatg agagacaata agtacaggtc cagtagatct cgaagtgttt tctacagact 840
gaccatactg atattagtat ttgctgttag ttggatgcc ctacaccttt tccatgtggg 900
aactgatttt aatgacaatc ttatttcaaa taggcatttc aagttgggtg attgcatttg 960
tcatttggtg ggcatgatgt cctgttgtct taatccaatt ctatatgggt ttcttaataa 1020
tggaattcag agagacttgc agttcttctt caacttttgt gatttccggt ctcgggatga 1080
tgattatgaa acaatagcca tgtccacgat gcacacagat gtttccaaaa cttctttgaa 1140
gcaagcaagc ccagtcgcat ttaaaaaaat caacaacaat gatgataatg aaaaaatctg 1200
a

```

```

<210> 9
<211> 499
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:Y5/Y1 CHIMERA

```

```

<400> 9
Met Ser Phe Tyr Ser Lys Gln Asp Tyr Asn Met Asp Leu Glu Leu Asp
 1             5             10            15

Glu Tyr Tyr Asn Lys Thr Leu Ala Thr Glu Asn Asn Thr Ala Ala Thr
      20             25             30

Arg Asn Ser Asp Phe Pro Val Trp Asp Asp Tyr Lys Ser Ser Val Asp
      35             40             45

Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu Leu
      50             55             60

Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Leu Met Lys Lys Arg
      65             70             75             80

Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser
      85             90             95

Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val
      100            105            110

Leu Leu Asp Gln Trp Met Phe Gly Lys Val Met Cys His Ile Met Pro
      115            120            125

Phe Leu Gln Cys Val Ser Val Leu Val Ser Thr Leu Ile Leu Ile Ser
      130            135            140

Ile Ala Ile Val Arg Tyr His Met Ile Lys His Pro Ile Ser Asn Asn
      145            150            155            160

```



Leu	Thr	Ala	Asn	His	Gly	Tyr	Phe	Leu	Ile	Ala	Thr	Val	Trp	Thr	Leu	
				165					170							
Gly	Phe	Ala	Ile	Cys	Ser	Pro	Leu	Pro	Val	Phe	His	Ser	Leu	Val	Glu	
				180					185							
Leu	Gln	Glu	Thr	Phe	Gly	Ser	Ala	Leu	Leu	Ser	Ser	Arg	Tyr	Leu	Cys	
				195					200							
Val	Glu	Ser	Trp	Pro	Ser	Asp	Ser	Tyr	Arg	Ile	Ala	Phe	Thr	Ile	Ser	
				210					215							
Leu	Leu	Leu	Val	Gln	Tyr	Ile	Leu	Pro	Leu	Val	Cys	Leu	Thr	Val	Ser	
				225					230							
His	Thr	Ser	Val	Cys	Arg	Ser	Ile	Ser	Cys	Gly	Leu	Ser	Asn	Lys	Glu	
				245					250							
Asn	Arg	Leu	Glu	Glu	Asn	Glu	Met	Ile	Asn	Leu	Thr	Leu	His	Pro	Ser	
				260					265							
Lys	Lys	Ser	Gly	Pro	Gln	Val	Lys	Leu	Ser	Gly	Ser	His	Lys	Trp	Ser	
				275					280							
Tyr	Ser	Phe	Ile	Lys	Lys	His	Arg	Arg	Arg	Tyr	Ser	Lys	Lys	Thr	Ala	
				290					295							
Cys	Val	Leu	Pro	Ala	Pro	Glu	Arg	Pro	Ser	Gln	Glu	Asn	His	Ser	Arg	
				305					310							
Ile	Leu	Pro	Glu	Asn	Phe	Gly	Ser	Val	Arg	Ser	Gln	Leu	Ser	Ser	Ser	
				325					330							
Ser	Lys	Phe	Ile	Pro	Gly	Val	Pro	Thr	Cys	Phe	Glu	Ile	Lys	Pro	Glu	
				340					345							
Glu	Asn	Ser	Asp	Val	His	Glu	Leu	Arg	Val	Lys	Arg	Ser	Val	Thr	Arg	
				355					360							
Ile	Lys	Lys	Arg	Ser	Arg	Ser	Val	Phe	Tyr	Arg	Leu	Thr	Ile	Leu	Ile	
				370					375							
Leu	Val	Phe	Ala	Val	Ser	Trp	Met	Pro	Leu	His	Leu	Phe	His	Val	Val	
				385					390							
Thr	Asp	Phe	Asn	Asp	Asn	Leu	Ile	Ser	Asn	Arg	His	Phe	Lys	Leu	Val	
				405					410							
Tyr	Cys	Ile	Cys	His	Leu	Leu	Gly	Met	Met	Ser	Cys	Cys	Leu	Asn	Pro	
				420					425							
Ile	Leu	Tyr	Gly	Phe	Leu	Asn	Asn	Gly	Ile	Gln	Arg	Asp	Leu	Gln	Phe	
				435					440							
Phe	Phe	Asn	Phe	Cys	Asp	Phe	Arg	Ser	Arg	Asp	Asp	Asp	Tyr	Glu	Thr	
				450					455							

Ile Ala Met Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys  
465 470 475 480

Gln Ala Ser Pro Val Ala Phe Lys Lys Ile Asn Asn Asn Asp Asp Asn  
485 490 495

Glu Lys Ile

$\langle 210 \rangle$  10

<211> 394

&lt;212&gt; PRT

<213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> Description of Artificial Sequence:Y5/Y1 CHIMERA

<400> 10

Met Ser Phe Tyr Ser Lys Gln Asp Tyr Asn Met Asp Leu Glu Leu Asp  
1 5 10 15

Glu Tyr Tyr Asn Lys Thr Leu Ala Thr Glu Asn Asn Thr Ala Ala Thr  
20 25 30

Arg Asn Ser Asp Phe Pro Val Trp Asp Asp Tyr Lys Ser Ser Val Asp  
35 40 45

Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu Leu  
50 55 60

Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Leu Met Lys Lys Arg  
65 70 75 80

Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser  
85 90 95

Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val  
 . 100 105 110

Leu Leu Asp Gln Trp Met Phe Gly Lys Val Met Cys His Ile Met Pro  
115 120 125

Phe Leu Gln Cys Val Ser Val Leu Val Ser Thr Leu Ile Leu Ile Ser  
130 135 140

Ile Ala Ile Val Arg Tyr His Met Ile Lys His Pro Ile Ser Asn Asn  
145 150 155 160

Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr Leu  
165 170 175

Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val Glu  
180 185 190

Leu Gln Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Arg Tyr Leu Cys

# 1. Introduction

195	200	205
Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile Ser 210 215 220		
Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu Val Cys Leu Thr Val Ser 225 230 235 240		
His Thr Ser Val Cys Ile Arg Leu Lys Arg Arg Asn Asn Met Met Asp 245 250 255		
Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser Arg Ser Arg Ser Val Phe 260 265 270		
Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp Met Pro 275 280 285		
Leu His Leu Phe His Val Val Thr Asp Phe Asn Asp Asn Leu Ile Ser 290 295 300		
Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu Leu Gly Met 305 310 315 320		
Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu Asn Asn Gly 325 330 335		
Ile Gln Arg Asp Leu Gln Phe Phe Phe Asn Phe Cys Asp Phe Arg Ser 340 345 350		
Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met Ser Thr Met His Thr Asp 355 360 365		
Val Ser Lys Thr Ser Leu Lys Gln Ala Ser Pro Val Ala Phe Lys Lys 370 375 380		
Ile Asn Asn Asn Asp Asp Asn Glu Lys Ile 385 390		

<210> 11

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HEXAHISTADINE  
TAG

<400> 11

His His His His His His  
1 5

<210> 12

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:FLAG EPITOPE  
TAG

<400> 12

Asp Tyr Lys Asp Asp Asp Asp Lys  
1 5

<210> 13

<211> 455

<212> PRT

<213> Homo sapiens

<400> 13

Met Ser Phe Tyr Ser Lys Gln Asp Tyr Asn Met Asp Leu Glu Leu Asp  
1 5 10 15

Glu Tyr Tyr Asn Lys Thr Leu Ala Thr Glu Asn Asn Thr Ala Ala Thr  
20 25 30

Arg Asn Ser Asp Phe Pro Val Trp Asp Asp Tyr Lys Ser Ser Val Asp  
35 40 45

Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu Leu  
50 55 60

Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Leu Met Lys Lys Arg  
65 70 75 80

Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser  
85 90 95

Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val  
100 105 110

Leu Leu Asp Gln Trp Met Phe Gly Lys Val Met Cys His Ile Met Pro  
115 120 125

Phe Leu Gln Cys Val Ser Val Leu Val Ser Thr Leu Ile Leu Ile Ser  
130 135 140

Ile Ala Ile Val Arg Tyr His Met Ile Lys His Pro Ile Ser Asn Asn  
145 150 155 160

Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr Leu  
165 170 175

Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val Glu  
180 185 190

Leu Gln Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Arg Tyr Leu Cys  
195 200 205

Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile Ser  
210 215 220

Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu Val Cys Leu Thr Val Ser  
 225 230 235 240  
 His Thr Ser Val Cys Arg Ser Ile Ser Cys Gly Leu Ser Asn Lys Glu  
 245 250 255  
 Asn Arg Leu Glu Glu Asn Glu Met Ile Asn Leu Thr Leu His Pro Ser  
 260 265 270  
 Lys Lys Ser Gly Pro Gln Val Lys Leu Ser Gly Ser His Lys Trp Ser  
 275 280 285  
 Tyr Ser Phe Ile Lys Lys His Arg Arg Arg Tyr Ser Lys Lys Thr Ala  
 290 295 300  
 Cys Val Leu Pro Ala Pro Glu Arg Pro Ser Gln Glu Asn His Ser Arg  
 305 310 315 320  
 Ile Leu Pro Glu Asn Phe Gly Ser Val Arg Ser Gln Leu Ser Ser Ser  
 325 330 335  
 Ser Lys Phe Ile Pro Gly Val Pro Thr Cys Phe Glu Ile Lys Pro Glu  
 340 345 350  
 Glu Asn Ser Asp Val His Glu Leu Arg Val Lys Arg Ser Val Thr Arg  
 355 360 365  
 Ile Lys Lys Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile  
 370 375 380  
 Leu Val Phe Ala Val Ser Trp Met Pro Leu His Leu Phe His Val Val  
 385 390 395 400  
 Thr Asp Phe Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val  
 405 410 415  
 Tyr Cys Ile Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro  
 420 425 430  
 Ile Leu Tyr Gly Phe Leu Asn Asn Gly Ile Lys Ala Asp Leu Val Ser  
 435 440 445  
 Leu Ile His Cys Leu His Met  
 450 455

<210> 14  
 <211> 21  
 <212> DNA  
 <213> Homo sapiens

<400> 14  
 ttttggttgc tgacaaatgt c

<210> 15

<211> 26  
<212> DNA  
<213> Homo sapiens

<400> 15  
ccttggtaaa cagtgagaat tattac

26

<210> 16  
<211> 63  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:CHIMERIC Y1/Y5  
PRIMER

<400> 16  
tacgcctaaa aaggagaaac aacatgatgg acaagatgag agacaataag tacagggtcca 60  
gta 63

<210> 17  
<211> 71  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:CHIMERIC Y1/Y5  
PRIMER

<400> 17  
gatctactgg acctgtactt attgtctctc atcttgtcca tcatgttggt tctccttttt 60  
aggcgtatgc a 71

<210> 18  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:MUTAGENIC R1  
PRIMER

<400> 18  
gaacaaaaga attcagagag acttgcagtt c

31

<210> 19  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:MUTAGENIC R1  
PRIMER

<400> 19  
cagcttgaat tccattatta agaaaccc

28

<210> 20  
<211> 341  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Y1/Y5 CHIMERA

<400> 20  
Met Asp Leu Glu Leu Gln Asp Phe Tyr Asn Lys Thr Leu Ala Thr Glu  
1 5 10 15  
Asn Asn Thr Ala Ala Thr Arg Asn Ser Asp Phe Pro Val Trp Asp Asp  
20 25 30  
Tyr Lys Ser Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr  
35 40 45  
Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met  
50 55 60  
Ala Leu Met Arg Lys Arg Asn Gln Lys Thr Met Val Asn Phe Leu Ile  
65 70 75 80  
Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro  
85 90 95  
Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe Gly Lys Val  
100 105 110  
Met Cys His Ile Met Pro Phe Leu Gln Cys Val Ser Val Leu Val Ser  
115 120 125  
Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys  
130 135 140  
His Pro Ile Ser Asn Asn Leu Thr Ala Asn His Gly Tyr Phe Leu Ile  
145 150 155 160  
Ala Thr Val Trp Thr Leu Gly Phe Ala Ile Cys Ser Pro Leu Pro Val  
165 170 175  
Phe His Ser Leu Val Glu Leu Gln Glu Thr Phe Asp Ser Ala Leu Leu  
180 185 190  
Ser Ser Arg Tyr Leu Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg  
195 200 205  
Ile Ala Phe Thr Ile Ser Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu  
210 215 220  
Val Cys Leu Thr Val Ser His Thr Ser Val Cys Ile Arg Leu Lys Arg

TrpAspTyrGlu

225                      230                      235                      240  
 Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser  
                                  245                      250                      255  
 Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe  
                                  260                      265                      270  
 Ala Val Ser Trp Met Pro Leu His Leu Phe His Val Val Thr Asp Phe  
                                  275                      280                      285  
 Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile  
                                  290                      295                      300  
 Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr  
 305                                   310                      315                      320  
 Gly Phe Leu Asn Asn Gly Ile Lys Ala Asp Leu Ile Ser Leu Ile Gln  
                                  325                      330                      335  
 Cys Leu His Met Ser  
                                  340

<210> 21  
 <211> 383  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Y1/Y5 CHIMERA

<400> 21  
 Met Asp Leu Glu Leu Gln Asp Phe Tyr Asn Lys Thr Leu Ala Thr Glu  
   1                                  5                                  10                                  15  
 Asn Asn Thr Ala Ala Thr Arg Asn Ser Asp Phe Pro Val Trp Asp Asp  
                                   20                                  25                                  30  
 Tyr Lys Ser Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr  
                                   35                                  40                                  45  
 Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met  
                                   50                                  55                                  60  
 Ala Leu Met Arg Lys Arg Asn Gln Lys Thr Met Val Asn Phe Leu Ile  
   65                                  70                                  75                                  80  
 Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro  
                                   85                                  90                                  95  
 Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe Gly Lys Val  
                                   100                                  105                                  110  
 Met Cys His Ile Met Pro Phe Leu Gln Cys Val Ser Val Leu Val Ser  
                                   115                                  120                                  125

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
841  
842  
843  
844  
845  
846  
847  
848  
849  
850  
851  
852  
853  
854  
855  
856  
857  
858  
859  
860  
861  
862  
863  
864  
865  
866  
867  
868  
869  
870  
871  
872  
873  
874  
875  
876  
877  
878  
879  
880  
881  
882  
883  
884  
885  
886  
887  
888  
889  
890  
891  
892  
893  
894  
895  
896  
897  
898  
899  
900  
901  
902  
903  
904  
905  
906  
907  
908  
909  
910  
911  
912  
913  
914  
915  
916  
917  
918  
919  
920  
921  
922  
923  
924  
925  
926  
927  
928  
929  
930  
931  
932  
933  
934  
935  
936  
937  
938  
939  
940  
941  
942  
943  
944  
945  
946  
947  
948  
949  
950  
951  
952  
953  
954  
955  
956  
957  
958  
959  
960  
961  
962  
963  
964  
965  
966  
967  
968  
969  
970  
971  
972  
973  
974  
975  
976  
977  
978  
979  
980  
981  
982  
983  
984  
985  
986  
987  
988  
989  
990  
991  
992  
993  
994  
995  
996  
997  
998  
999  
1000



Thr	Leu	Ile	Leu	Ile	Ser	Ile	Ala	Ile	Val	Arg	Tyr	His	Met	Ile	Lys	130	135	140
His	Pro	Ile	Ser	Asn	Asn	Leu	Thr	Ala	Asn	His	Gly	Tyr	Phe	Leu	Ile	145	150	155
Ala	Thr	Val	Trp	Thr	Leu	Gly	Phe	Ala	Ile	Cys	Ser	Pro	Leu	Pro	Val	165	170	175
Phe	His	Ser	Leu	Val	Glu	Leu	Gln	Glu	Thr	Phe	Asp	Ser	Ala	Leu	Leu	180	185	190
Ser	Ser	Arg	Tyr	Leu	Cys	Val	Glu	Ser	Trp	Pro	Ser	Asp	Ser	Tyr	Arg	195	200	205
Ile	Ala	Phe	Thr	Ile	Ser	Leu	Leu	Leu	Val	Gln	Tyr	Ile	Leu	Pro	Leu	210	215	220
Val	Cys	Leu	Thr	Val	Ser	His	Thr	Ser	Val	Cys	Ile	Arg	Leu	Lys	Arg	225	230	235
Arg	Asn	Asn	Met	Met	Asp	Lys	Met	Arg	Asp	Asn	Lys	Tyr	Arg	Ser	Ser	245	250	255
Arg	Ser	Arg	Ser	Val	Phe	Tyr	Arg	Leu	Thr	Ile	Leu	Ile	Leu	Val	Phe	260	265	270
Ala	Val	Ser	Trp	Met	Pro	Leu	His	Leu	Phe	His	Val	Val	Thr	Asp	Phe	275	280	285
Asn	Asp	Asn	Leu	Ile	Ser	Asn	Arg	His	Phe	Lys	Leu	Val	Tyr	Cys	Ile	290	295	300
Cys	His	Leu	Leu	Gly	Met	Met	Ser	Cys	Cys	Leu	Asn	Pro	Ile	Leu	Tyr	305	310	315
Gly	Phe	Leu	Asn	Asn	Gly	Ile	Gln	Arg	Asp	Leu	Gln	Phe	Phe	Phe	Asn	325	330	335
Phe	Cys	Asp	Phe	Arg	Ser	Arg	Asp	Asp	Asp	Tyr	Glu	Thr	Ile	Ala	Met	340	345	350
Ser	Thr	Met	His	Thr	Asp	Val	Ser	Lys	Thr	Ser	Leu	Lys	Gln	Ala	Ser	355	360	365
Pro	Val	Ala	Phe	Lys	Lys	Ile	Asn	Asn	Asp	Asp	Asn	Glu	Lys	Ile		370	375	380

<210> 22

<211> 508

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Y1/Y5 CHIMERA

# THE FUTURE OF THE FUTURE

Met	Glu	Val	Lys	Leu	Glu	Glu	His	Phe	Asn	Lys	Thr	Phe	Val	Thr	Glu
1				5					10					15	
Asn	Asn	Thr	Ala	Ala	Ser	Gln	Asn	Thr	Ala	Ser	Pro	Ala	Trp	Glu	Asp
			20					25					30		
Tyr	Arg	Gly	Thr	Glu	Asn	Asn	Thr	Ser	Ala	Ala	Arg	Asn	Thr	Ala	Phe
		35					40					45			
Pro	Val	Trp	Glu	Asp	Tyr	Arg	Gly	Ser	Val	Asp	Asp	Leu	Gln	Tyr	Phe
	50					55				60					
Leu	Ile	Gly	Leu	Tyr	Thr	Phe	Val	Ser	Leu	Leu	Gly	Phe	Met	Gly	Asn
65					70					75					80
Leu	Leu	Ile	Leu	Met	Ala	Val	Met	Lys	Lys	Arg	Asn	Gln	Lys	Thr	Thr
				85					90					95	
Val	Asn	Phe	Leu	Ile	Gly	Asn	Leu	Ala	Phe	Ser	Asp	Ile	Leu	Val	Val
			100					105					110		
Leu	Phe	Cys	Ser	Pro	Phe	Thr	Leu	Thr	Ser	Val	Leu	Leu	Asp	Gln	Trp
		115					120					125			
Met	Phe	Gly	Lys	Ala	Met	Cys	His	Ile	Met	Pro	Phe	Leu	Gln	Cys	Val
	130					135					140				
Ser	Val	Leu	Val	Ser	Thr	Leu	Ile	Leu	Ile	Ser	Ile	Ala	Ile	Val	Arg
145					150					155					160
Tyr	His	Met	Ile	Lys	His	Pro	Ile	Ser	Asn	Asn	Leu	Thr	Ala	Asn	His
				165					170					175	
Gly	Tyr	Phe	Leu	Ile	Ala	Thr	Val	Trp	Thr	Leu	Gly	Phe	Ala	Ile	Cys
			180					185					190		
Ser	Pro	Phe	Pro	Val	Phe	His	Ser	Leu	Val	Glu	Leu	Lys	Glu	Thr	Phe
		195					200					205			
Gly	Ser	Ala	Leu	Leu	Ser	Ser	Lys	Tyr	Leu	Cys	Val	Glu	Ser	Trp	Pro
	210					215					220				
Ser	Asp	Ser	Tyr	Arg	Ile	Ala	Phe	Thr	Ile	Ser	Leu	Leu	Leu	Val	Gln
225					230					235					240
Tyr	Ile	Leu	Pro	Leu	Val	Cys	Leu	Thr	Val	Ser	His	Thr	Ser	Val	Cys
				245					250					255	
Arg	Ser	Ile	Ser	Cys	Gly	Leu	Ser	His	Lys	Glu	Asn	Arg	Leu	Glu	Glu
			260					265					270		
Asn	Glu	Met	Ile	Asn	Leu	Thr	Leu	His	Pro	Ser	Lys	Lys	Ser	Arg	Asp
		275					280					285			
Gln	Ala	Lys	Pro	Pro	Ser	Thr	Gln	Lys	Trp	Ser	Tyr	Ser	Phe	Ile	Arg
	290					295					300				

Lys His Arg Arg Arg Tyr Ser Lys Lys Thr Ala Cys Val Leu Pro Ala  
 305 310 315 320  
 Pro Ala Gly Pro Ser Gln Glu Lys His Leu Thr Val Pro Glu Asn Pro  
 325 330 335  
 Gly Ser Val Arg Ser Gln Leu Ser Pro Ser Ser Lys Val Ile Pro Gly  
 340 345 350  
 Val Pro Ile Cys Phe Glu Val Lys Pro Glu Glu Ser Ser Asp Ala Gln  
 355 360 365  
 Glu Met Arg Val Lys Arg Ser Leu Thr Arg Ile Lys Lys Arg Ser Arg  
 370 375 380  
 Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser  
 385 390 395 400  
 Trp Met Pro Leu His Val Phe His Val Val Thr Asp Phe Asn Asp Asn  
 405 410 415  
 Leu Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu  
 420 425 430  
 Leu Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu  
 435 440 445  
 Asn Asn Gly Ile Gln Arg Asp Leu Gln Phe Phe Phe Asn Phe Cys Asp  
 450 455 460  
 Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met Ser Thr Met  
 465 470 475 480  
 His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser Pro Val Ala  
 485 490 495  
 Phe Lys Lys Ile Ser Met Asn Asp Asn Glu Lys Val  
 500 505

<210> 23

<211> 352

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Y1/Y5 CHIMERA

<400> 23

Met Asp Val Leu Phe Phe His Gln Asp Ser Ser Met Glu Phe Lys Leu  
 1 5 10 15

Glu Glu His Phe Asn Lys Thr Phe Val Thr Glu Asn Asn Thr Ala Ala  
 20 25 30

Ala Arg Asn Ala Ala Phe Pro Ala Trp Glu Asp Tyr Arg Gly Ser Val



&lt;210&gt; 24

&lt;211&gt; 499

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:Y1/Y5 CHIMERA

&lt;400&gt; 24

Met	Asp	Val	Leu	Phe	Phe	His	Gln	Asp	Ser	Ser	Met	Glu	Phe	Lys	Leu
1				5					10					15	

Glu	Glu	His	Phe	Asn	Lys	Thr	Phe	Val	Thr	Glu	Asn	Asn	Thr	Ala	Ala
			20					25					30		

Ala	Arg	Asn	Ala	Ala	Phe	Pro	Ala	Trp	Glu	Asp	Tyr	Arg	Gly	Ser	Val
		35					40					45			

Asp	Asp	Leu	Gln	Tyr	Phe	Leu	Ile	Gly	Leu	Tyr	Thr	Phe	Val	Ser	Leu
	50					55					60				

Leu	Gly	Phe	Met	Gly	Asn	Leu	Leu	Ile	Leu	Met	Ala	Val	Met	Lys	Lys
65					70					75					80

Arg	Asn	Gln	Lys	Thr	Thr	Val	Asn	Phe	Leu	Ile	Gly	Asn	Leu	Ala	Phe
				85					90					95	

Ser	Asp	Ile	Leu	Val	Val	Leu	Phe	Cys	Ser	Pro	Phe	Thr	Leu	Thr	Ser
			100					105					110		

Val	Leu	Leu	Asp	Gln	Trp	Met	Phe	Gly	Lys	Ala	Met	Cys	His	Ile	Met
		115					120					125			

Pro	Phe	Leu	Gln	Cys	Val	Ser	Val	Leu	Val	Ser	Thr	Leu	Ile	Leu	Ile
		130				135					140				

Ser	Ile	Ala	Ile	Val	Arg	Tyr	His	Met	Ile	Lys	His	Pro	Ile	Ser	Asn
145					150					155					160

Asn	Leu	Thr	Ala	Asn	His	Gly	Tyr	Phe	Leu	Ile	Ala	Thr	Val	Trp	Thr
			165						170					175	

Leu	Gly	Phe	Ala	Ile	Cys	Ser	Pro	Leu	Pro	Val	Phe	His	Ser	Leu	Val
			180					185					190		

Glu	Leu	Lys	Glu	Thr	Phe	Gly	Ser	Ala	Leu	Leu	Ser	Ser	Lys	Tyr	Leu
		195					200					205			

Cys	Val	Glu	Ser	Trp	Pro	Ser	Asp	Ser	Tyr	Arg	Ile	Ala	Phe	Thr	Ile
		210				215					220				

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400

Ser	Leu	Leu	Leu	Val	Gln	Tyr	Ile	Leu	Pro	Leu	Val	Cys	Leu	Thr	Val	225	230	235	240
Ser	His	Thr	Ser	Val	Cys	Arg	Ser	Ile	Ser	Cys	Gly	Leu	Ser	His	Lys	245	250	255	
Glu	Asn	Arg	Leu	Glu	Glu	Asn	Glu	Met	Ile	Asn	Leu	Thr	Leu	Gln	Pro	260	265	270	
Ser	Lys	Lys	Ser	Arg	Asn	Gln	Ala	Lys	Thr	Pro	Ser	Thr	Gln	Lys	Trp	275	280	285	
Ser	Tyr	Ser	Phe	Ile	Arg	Lys	His	Arg	Arg	Arg	Tyr	Ser	Lys	Lys	Thr	290	295	300	
Ala	Cys	Val	Leu	Pro	Ala	Pro	Ala	Gly	Pro	Ser	Gln	Gly	Lys	His	Leu	305	310	315	320
Ala	Val	Pro	Glu	Asn	Pro	Ala	Ser	Val	Arg	Ser	Gln	Leu	Ser	Pro	Ser	325	330	335	
Ser	Lys	Val	Ile	Pro	Gly	Val	Pro	Ile	Cys	Phe	Glu	Val	Lys	Pro	Glu	340	345	350	
Glu	Ser	Ser	Asp	Ala	His	Glu	Met	Arg	Val	Lys	Arg	Ser	Ile	Thr	Arg	355	360	365	
Ile	Lys	Lys	Arg	Ser	Arg	Ser	Val	Phe	Tyr	Arg	Leu	Thr	Ile	Leu	Ile	370	375	380	
Leu	Val	Phe	Ala	Val	Ser	Trp	Met	Pro	Leu	His	Val	Phe	His	Val	Val	385	390	395	400
Thr	Asp	Phe	Asn	Asp	Asn	Leu	Ile	Ser	Asn	Arg	His	Phe	Lys	Leu	Val	405	410	415	
Tyr	Cys	Ile	Cys	His	Leu	Leu	Gly	Met	Met	Ser	Cys	Cys	Leu	Asn	Pro	420	425	430	
Ile	Leu	Tyr	Gly	Phe	Leu	Asn	Asn	Gly	Ile	Lys	Gln	Arg	Asp	Leu	Gln	435	440	445	
Phe	Phe	Phe	Asn	Phe	Cys	Asp	Phe	Arg	Ser	Arg	Asp	Asp	Asp	Tyr	Glu	450	455	460	
Thr	Ile	Ala	Met	Ser	Thr	Met	His	Thr	Asp	Val	Ser	Lys	Thr	Ser	Leu	465	470	475	480
Lys	Gln	Ala	Ser	Pro	Val	Ala	Phe	Lys	Lys	Ile	Ser	Met	Asn	Asp	Asn	485	490	495	
Glu	Lys	Ile																	

<210> 25  
<211> 395



Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp Met  
           275                          280                          285  
 Pro Leu His Val Phe His Val Val Thr Asp Phe Asn Asp Asn Leu Ile  
           290                          295                          300  
 Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu Leu Gly  
 305                          310                          315                          320  
 Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu Asn Asn  
                           325                          330                          335  
 Gly Ile Lys Gln Arg Asp Leu Gln Phe Phe Phe Asn Phe Cys Asp Phe  
                           340                          345                          350  
 Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met Ser Thr Met His  
                           355                          360                          365  
 Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser Pro Val Ala Phe  
           370                          375                          380  
 Lys Lys Ile Ser Met Asn Asp Asn Glu Lys Ile  
 385                          390                          395

<210> 26  
 <211> 341  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Y1/Y5 CHIMERA

<400> 26  
 Met Gly Ser Glu Ile Pro Asp Tyr Tyr Asn Lys Thr Leu Ala Ser Glu  
   1                          5                          10                          15  
 Asn Asn Thr Val Ala Thr Arg Asn Ser Gly Phe Pro Val Trp Glu Asp  
           20                          25                          30  
 Tyr Lys Gly Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr  
           35                          40                          45  
 Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met  
           50                          55                          60  
 Ala Val Met Arg Lys Arg Asn Gln Lys Thr Thr Val Asn Phe Leu Ile  
           65                          70                          75                          80  
 Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro  
                           85                          90                          95  
 Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe Gly Lys Val  
           100                          105                          110  
 Met Cys His Ile Met Pro Phe Leu Gln Cys Val Thr Val Leu Val Ser



115					120					125					
Thr	Leu	Ile	Leu	Ile	Ser	Ile	Ala	Ile	Val	Arg	Tyr	His	Met	Ile	Lys
130					135					140					
His	Pro	Val	Ser	Asn	Asn	Leu	Thr	Ala	Asn	His	Gly	Tyr	Phe	Leu	Ile
145				150						155					160
Ala	Thr	Val	Trp	Thr	Leu	Gly	Leu	Ala	Ile	Cys	Ser	Pro	Leu	Pro	Val
				165					170					175	
Phe	His	Ser	Leu	Val	Glu	Leu	Gln	Glu	Ser	Phe	Gly	Ser	Ala	Trp	Leu
			180				185						190		
Ser	Ser	Arg	Tyr	Leu	Cys	Val	Glu	Ser	Trp	Pro	Ser	Asp	Ser	Tyr	Arg
		195					200					205			
Ile	Ala	Phe	Thr	Ile	Ser	Leu	Leu	Val	Gln	Tyr	Ile	Leu	Pro	Leu	
	210					215					220				
Val	Cys	Leu	Thr	Val	Ser	His	Thr	Ser	Val	Cys	Ile	Arg	Leu	Lys	Arg
225				230						235				240	
Arg	Asn	Asn	Met	Met	Asp	Lys	Met	Arg	Asp	Asn	Lys	Tyr	Arg	Ser	Ser
			245						250					255	
Arg	Ser	Arg	Ser	Val	Phe	Tyr	Arg	Leu	Thr	Val	Leu	Ile	Leu	Val	Phe
			260					265					270		
Ala	Val	Ser	Trp	Met	Pro	Leu	His	Leu	Phe	His	Val	Val	Thr	Asp	Phe
			275				280						285		
Asn	Asp	Asn	Leu	Ile	Ser	Asn	Arg	His	Phe	Lys	Leu	Val	Tyr	Cys	Ile
	290					295					300				
Cys	His	Leu	Leu	Gly	Met	Met	Ser	Cys	Cys	Leu	Asn	Pro	Ile	Leu	Tyr
305				310						315					320
Gly	Phe	Leu	Asn	Asn	Gly	Ile	Lys	Ala	Asp	Leu	Met	Ser	Leu	Ile	His
			325						330					335	
Cys	Leu	His	Val	Ser											
			340												

<210> 27

<211> 383

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Y1/Y5 CHIMERA

<400> 27

Met	Gly	Ser	Glu	Ile	Pro	Asp	Tyr	Tyr	Asn	Lys	Thr	Leu	Ala	Ser	Glu
1				5					10					15	

Asn	Asn	Thr	Val	Ala	Thr	Arg	Asn	Ser	Gly	Phe	Pro	Val	Trp	Glu	Asp	20	25	30
Tyr	Lys	Gly	Ser	Val	Asp	Asp	Leu	Gln	Tyr	Phe	Leu	Ile	Gly	Leu	Tyr	35	40	45
Thr	Phe	Val	Ser	Leu	Leu	Gly	Phe	Met	Gly	Asn	Leu	Leu	Ile	Leu	Met	50	55	60
Ala	Val	Met	Arg	Lys	Arg	Asn	Gln	Lys	Thr	Thr	Val	Asn	Phe	Leu	Ile	65	70	75
Gly	Asn	Leu	Ala	Phe	Ser	Asp	Ile	Leu	Val	Val	Leu	Phe	Cys	Ser	Pro	85	90	95
Phe	Thr	Leu	Thr	Ser	Val	Leu	Leu	Asp	Gln	Trp	Met	Phe	Gly	Lys	Val	100	105	110
Met	Cys	His	Ile	Met	Pro	Phe	Leu	Gln	Cys	Val	Thr	Val	Leu	Val	Ser	115	120	125
Thr	Leu	Ile	Leu	Ile	Ser	Ile	Ala	Ile	Val	Arg	Tyr	His	Met	Ile	Lys	130	135	140
His	Pro	Val	Ser	Asn	Asn	Leu	Thr	Ala	Asn	His	Gly	Tyr	Phe	Leu	Ile	145	150	155
Ala	Thr	Val	Trp	Thr	Leu	Gly	Leu	Ala	Ile	Cys	Ser	Pro	Leu	Pro	Val	165	170	175
Phe	His	Ser	Leu	Val	Glu	Leu	Gln	Glu	Ser	Phe	Gly	Ser	Ala	Trp	Leu	180	185	190
Ser	Ser	Arg	Tyr	Leu	Cys	Val	Glu	Ser	Trp	Pro	Ser	Asp	Ser	Tyr	Arg	195	200	205
Ile	Ala	Phe	Thr	Ile	Ser	Leu	Leu	Leu	Val	Gln	Tyr	Ile	Leu	Pro	Leu	210	215	220
Val	Cys	Leu	Thr	Val	Ser	His	Thr	Ser	Val	Cys	Ile	Arg	Leu	Lys	Arg	225	230	235
Arg	Asn	Asn	Met	Met	Asp	Lys	Met	Arg	Asp	Asn	Lys	Tyr	Arg	Ser	Ser	245	250	255
Arg	Ser	Arg	Ser	Val	Phe	Tyr	Arg	Leu	Thr	Val	Leu	Ile	Leu	Val	Phe	260	265	270
Ala	Val	Ser	Trp	Met	Pro	Leu	His	Leu	Phe	His	Val	Val	Thr	Asp	Phe	275	280	285
Asn	Asp	Asn	Leu	Ile	Ser	Asn	Arg	His	Phe	Lys	Leu	Val	Tyr	Cys	Ile	290	295	300
Cys	His	Leu	Leu	Gly	Met	Met	Ser	Cys	Cys	Leu	Asn	Pro	Ile	Leu	Tyr	305	310	315
																		320

Protein Data Bank





Tyr Cys Ile Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro  
 420 425 430

Ile Leu Tyr Gly Phe Leu Asn Asn Gly Ile Lys Ala Asp Leu Met Ser  
 435 440 445

Leu Ile His Cys Leu His Met  
 450 455

<210> 31  
 <211> 1406  
 <212> DNA  
 <213> Cercopithecus aethiops

<400> 31  
 ttttggttgc tgacaaatgt ctttttattc caagcaggac tataatatgg atttagagct 60  
 tgatgaatat tataacaaga cacttgccac agagaataat actgctgccca ctcggaattc 120  
 tgatttccca gtctgggatg actataaaaag cagtgtagat gacttacagt attttctgat 180  
 tgggctctat acatttgtaa gtcttcttgg ctttatgggg aatttactta ttttaattgc 240  
 tctcatgaaa aagcgtaatc agaagactac ggtaaaacttc cttataggaa atctggcctt 300  
 ttctgacatc ttggttggtc tgttttgctc acctttcaca ctgacgtctg tcttgctgga 360  
 tcagtggatg tttggcaaag tcatgtgccca tattatgcct tttctgcaat gtgtgtcagt 420  
 tttggtttca actttaattt taatatcaat tgccattgtc aggtatcata tgataaaaca 480  
 tcccatctct aataatttaa cagcaaacca tggctacttt ctgatagcta ctgtctggac 540  
 actaggtttt gccatctggt ctccccttcc agtggttcac agtcttggg aacttcaaga 600  
 aacatttggt tcagcgttgc tgagcagcag gtatttatgt gttgagtcac ggccatctga 660  
 ttcatacaga attgccttta ctatctcttt attgctagtt cagtatatc tgcccttagt 720  
 ttgtcttact gtaagtcata caagtgtctg cagaagcata agctgtggat tgtccaacaa 780  
 agaaaacaga cttgaagaaa acgagatgat caacttaact cttcatccat ctagaaagat 840  
 tgggcctcag gtgaaactct ctggcagcca taaatggagt tattcattca tcaaaaaaca 900  
 cagaaggaga tatagcaaga agacagcatg tgtgttacct gctccagaaa gaccttctca 960  
 agagaaccac tccagaatac ttccagaaaa ctttggtctt gtaagaagtc agctctcttc 1020  
 atccagtaag ttcataccag gggctccccc ttgctttgaa ataaaaacct aagaaaattc 1080  
 agatgttcat gaattgagag taaaacgttc tgttacaaga ataaaaaaga gatctcgaag 1140  
 tgttttctac aggctgacca tactgatact agtatttgcg gtttagttgga tgccactaca 1200  
 ccttttccat gtggtaactg attttaatga caatcttatt tcaaataaggc atttcaagtt 1260  
 ggtgtattgc atttgtcatt tgttgggcat gatgtcctgt tgtcttaatc caattctgta 1320  
 tggatttctt aataatggga ttaaagctga tttaatgtct cttatacact gtcttcatat 1380  
 gtaataattc tcactgttta ccaagg 1406